

Gene Section

Mini Review

CREB3L2 (cAMP responsive element binding protein 3-like 2)

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Published in Atlas Database: October 2004

Online updated version : <http://AtlasGeneticsOncology.org/Genes/CREB3L2ID153ch7q33.html>

DOI: 10.4267/2042/38130

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Identity

Other names:

BBF2H7 (BBF2 human homolog on chromosome 7);
DKFZp586F2423; DKFZp686O19165;
TCAG_1951439

HGNC (Hugo):

CREB3L2

Location: 7q34

Note:

(position on chromosome 7 sequence according to UCSC database: 137021995-137144058).

DNA/RNA

Description

122,064 Kb, 12 exons. Exon 1, containing the initiation ATG, is the largest (454 bp) and exon 7 the smallest (59 bp). Exon 12 includes the termination TAA codon. Introns 1 and 9 are the largest (73132 bp) and smallest (281 bp), respectively.

Transcription

The strongest expression was seen in placenta, lung, spleen and intestine, and the weakest in heart, brain, skeletal muscle, thymus, colon and leukocytes. In fetal tissues, the weakest expression was detected in brain and heart. A splice variant, lacking exon 2, was found in placenta, spleen and fetal liver.

Protein

Description

519 amino acids, 57 kDa. The amino acid sequence

spanning residues 291-356 of the predicted human CREB3L2 protein contains a consensus B-ZIP domain highly similar to that in the CREB3L1, CREB3L3, CREB3L4, CREB3 and Drosophila Bbf-2 transcription factors with 80, 60, 59, 56 and 71% identity, respectively. It also contains the amino acid sequence RRKKKEY which is exactly conserved among CREB, CREM, ATF1, ATF6 and CREBL1. The leucine zipper motif of CREB3L2 is similar to that in CREB3L3 and CREB3L4 (pattern L-X6-C-X6-L-X6-L-X6-L-X6-L). It contains six repeats and consists of five leucines and one cysteine at the second heptad position (amino acid 328) of the leucine zipper. Downstream of the B-ZIP domain, CREB3L2 also contains a hydrophobic region, which was predicted to be an α -helical transmembrane domain (position 376-397; GTCLMVVVLCFVAFAFGSFFQGY) by the prediction program PSORT II. This structural feature is also seen in the other members of the family, i.e. CREB3L1, CREB3L3, CREB3 and CREB3L4.

Function

B-ZIP transcription factor.

Homology

CREB3L2 is a member of the old astrocyte specifically induced substance (OASIS) DNA binding and basic leucine zipper dimerization (B-ZIP) family of transcription factors, together with CREB3L1 (also known as OASIS), CREB3L3, CREB3 and CREB3L4.

Implicated in

Disease

Low-grade fibromyxoid sarcoma (LGFMS), variant of fibrosarcoma.

Prognosis

Usually cured by surgical excision, but may metastasize in up to 10% of the cases.

Cytogenetics

t(7;16)(q33-34;p11) or more complex rearrangements involving 7q and 16p. Some cases show the presence of supernumerary ring chromosomes without any detectable breakpoint in 7q or 16p.

Hybrid/Mutated gene

The most common transcripts are due to fusion of exon 6 or 7 with exon 5 of FUS and CREB3L2, respectively. The breakpoints in the fusion transcripts so far reported have, however, varied from exon 5-7 of FUS and from intron 4 to exon 6 of CREB3L2.

Abnormal protein

FUS/CREB3L2. The chimera is coding for a protein containing the N-terminus of FUS, and the B-ZIP domain and the C-terminus of CREB3L2. In the FUS/CREB3L2 chimera, the bZIP-encoding domain of CREB3L2 comes under the control of the FUS promoter, which, in turn, may cause deregulation of genes normally controlled by CREB3L2.

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This article should be referenced as such:

Storlazzi CT, Mertens F, Panagopoulos I. CREB3L2 (cAMP responsive element binding protein 3-like 2). *Atlas Genet Cytogenet Oncol Haematol.* 2004; 8(4):316-317.
